


SEQUENCE LISTING

(1) GENERAL INFORMATION:

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- (i) APPLICANT: Lee, Jong Y.
 - (ii) TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
 - (iii) NUMBER OF SEQUENCES: 5
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C., P.A.
 - (B) STREET: 60 South Sixth Street, Suite 3300
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/016,159
 - (B) FILING DATE: 30-JAN-1998
 - (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/876,227
 - (B) FILING DATE: 16-JUN-1997
 - (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/734,097
 - (B) FILING DATE: 21-OCT-1996
 - (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/460,525
 - (B) FILING DATE: 02-JUN-1995
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ellinger, Mark S.
 - (B) REGISTRATION NUMBER: 34,812
 - (C) REFERENCE/DOCKET NUMBER: 07004/002004
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612/335-5070
 - (B) TELEFAX: 612/288-9696

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: BamH1 linker ar 5' end followed by sequence for amino acids 25 through 29 of the full length human Epor protein. Forward primer for Sequence ID No. 2."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGATCC GCG CCC CCG CCT A AC
Ala Pro Pro Pro
1

23

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: EcoR1 linker followed by sequence complementary to coding sequence for amino acids 226 through 222 of full length human Epor protein. Reverse primer for Sequence ID No. 1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGAATTCGGG GTCCAGGTCG CT

22

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: pGEX-2T, Pharmacia (Mechanicsburg, PA)

(ix) FEATURE:
 (A) NAME/KEY: Thrombin Cleavage Site in plasmid vector pGEX-2T."

(x) PUBLICATION INFORMATION:
 (A) AUTHORS: Smith, D.B.
 Johnson, K.S.
 (B) TITLE: Single-step purification of polypeptides
 expressed in Escherichia coli as fusions with
 glutathione-S-transferase
 (D) VOLUME: 67
 (F) PAGES: 31-40
 (G) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTG GTT CCG CGT GGA T CC	18
Leu Val Pro Arg Gly	
5	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1527 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(x) PUBLICATION INFORMATION:
 (A) AUTHORS: Winkelmann , J. C., et al.
 (C) JOURNAL: Blood
 (D) VOLUME: 76
 (E) ISSUE: 1
 (F) PAGES: 24-30
 (G) DATE: 1990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG GAC CAC CTC GGG GCG TCC CTC TGG CCC CAG GTC GGC TCC CTT TGT	48
Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys	
1 5 10 15	
CTC CTG CTC GCT GGG GCC GCC TGG GCG CCC CCG CCT AAC CTC CCG GAC	96
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp	
20 25 30	
CCC AAG TTC GAG AGC AAA GCG GCC TTG CTG GCG GCC CGG GGG CCC GAA	144
Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu	
35 40 45	
GAG CTT CTG TGC TTC ACC GAG CGG TTG GAG GAC TTG GTG TGT TTC TGG	192
Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp	
50 55 60	
GAG GAA GCG GCG AGC GCT GGG GTG GGC CCG GGC AAC TAC AGC TTC TCC	240
Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser	
65 70 75 80	
TAC CAG CTC GAG GAT GAG CCA TGG AAG CTG TGT CGC CTG CAC CAG GCT	288
Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala	
85 90 95	

CCC Pro	ACG Thr	GCT Ala	CGT Arg 100	GGT Gly	CGG Arg	GTG Val	CGC Arg	TTC Phe 105	TGG Trp	TGT Cys	TCG Ser	CTG Leu	CCT Pro 110	ACA Thr	GCC Ala	336
GAC Asp	ACG Thr	TCG Ser 115	AGC Ser	TTC Phe	GTG Val	CCC Pro	CTA Leu 120	GAG Glu	TTG Leu	CGC Arg	GTC Val	ACA Thr 125	GCA Ala	GCC Ala	TCC Ser	384
GGC Gly	GCT Ala 130	CCG Pro	CGA Arg	TAT Tyr	CAC His	CGT Arg 135	GTC Val	ATC Ile	CAC His	ATC Ile	AAT Asn 140	GAA Glu	GTA Val	GTG Val	CTC Leu	432
CTA Leu 145	GAC Asp	GCC Ala	CCC Pro	GTG Val	GGG Gly 150	CTG Leu	GTG Val	GCG Ala	CGG Arg	TTG Leu 155	GCT Ala	GAC Asp	GAG Glu	AGC Ser	GGC Gly 160	480
CAC His	GTA Val	GTG Val	TTG Leu	CGC Arg 165	TGG Trp	CTC Leu	CCG Pro	CCG Pro	CCT Pro 170	GAG Glu	ACA Thr	CCC Pro	ATG Met	ACG Thr 175	TCT Ser	528
CAC His	ATC Ile	CGC Arg	TAC Tyr 180	GAG Glu	GTG Val	GAC Asp	GTC Val	TCG Ser 185	GCC Ala	GGC Gly	AAC Asn	CGG Arg	CCA Pro 190	GGG Gly	AGC Ser	576
GTA Val	CAG Gln 195	AGG Arg	GTG Val	GAG Glu	ATC Ile	CTG Leu	GAG Glu 200	GGC Gly	CGC Arg	ACC Thr	GAG Glu 205	TGT Cys	GTG Val	CTG Leu	AGC Ser	624
AAC Asn 210	CTG Leu	CGG Arg	GGC Gly	CGG Arg	ACG Thr	CGC Arg 215	TAC Tyr	ACC Thr	TTC Phe	GCC Ala	GTC Val 220	CGC Arg	GCG Ala	CGT Arg	ATG Met	672
GCT Ala 225	GAG Glu	CCG Pro	AGC Ser	TTC Phe	GGC Gly 230	GGC Gly	TTC Phe	TGG Trp	AGC Ser	GCC Ala 235	TGG Trp	TCG Ser	GAG Glu	CCT Pro	GTG Val 240	720
TCG Ser	CTG Leu	CTG Leu	GAG Glu	CCT Pro 245	AGC Ser	GAC Asp	CTG Leu	GAC Asp	CCC Pro 250	CTC Leu	ATC Ile	CTG Leu	ACG Thr 255	CTC Leu	TCC Ser	768
CTC Leu	ATC Ile	CTC Leu	GTG Val 260	GTC Val	ATC Ile	CTG Leu	GTG Val 265	CTG Leu	CTG Leu	ACC Thr	GTG Val	CTC Leu	GCG Ala 270	CTG Leu	CTC Leu	816
TCC Ser	CAC His	CGC Arg 275	CGG Arg	GCT Ala	CTG Leu	AAG Lys	CAG Gln 280	AAG Lys	ATC Ile	TGG Trp	CCT Pro	GGC Gly 285	ATC Ile	CCG Pro	AGC Ser	864
CCA Pro	GAG Glu 290	AGC Ser	GAG Glu	TTT Phe	GAA Glu	GGC Gly 295	CTC Leu	TTC Phe	ACC Thr	ACC Thr	CAC His 300	AAG Lys	GGT Gly	AAC Asn	TTC Phe	912
CAG Gln 305	CTG Leu	TGG Trp	CTG Leu	TAC Tyr	CAG Gln 310	AAT Asn	GAT Asp	GGC Gly	TGC Cys	CTG Leu 315	TGG Trp	TGG Trp	AGC Ser	CCC Pro	TGC Cys 320	960
ACC Thr	CCC Pro	TTC Phe	ACG Thr	GAG Glu 325	GAC Asp	CCA Pro	CCT Pro	GCT Ala	TCC Ser 330	CTG Leu	GAA Glu	GTC Val	CTC Leu	TCA Ser 335	GAG Glu	1008
CGC Arg	TGC Cys	TGG Trp	GGG Gly	ACG Thr	ATG Met	CAG Gln	GCA Ala	GTG Val	GAG Glu	CCG Pro	GGG Gly	ACA Thr	GAT Asp	GAT Asp	GAG Glu	1056

340					345					350						
GGC	CCC	CTG	CTG	GAG	CCA	GTG	GGC	AGT	GAG	CAT	GCC	CAG	GAT	ACC	TAT	1104
Gly	Pro	Leu	Leu	Glu	Pro	Val	Gly	Ser	Glu	His	Ala	Gln	Asp	Thr	Tyr	
		355					360					365				
CTG	GTG	CTG	GAC	AAA	TGG	TTG	CTG	CCC	CGG	AAC	CCG	CCC	AGT	GAG	GAC	1152
Leu	Val	Leu	Asp	Lys	Trp	Leu	Leu	Pro	Arg	Asn	Pro	Pro	Ser	Glu	Asp	
	370					375					380					
CTC	CCA	GGG	CCT	GGT	GGC	AGT	GTG	GAC	ATA	GTG	GCC	ATG	GAT	GAA	GGC	1200
Leu	Pro	Gly	Pro	Gly	Gly	Ser	Val	Asp	Ile	Val	Ala	Met	Asp	Glu	Gly	
	385				390					395					400	
TCA	GAA	GCA	TCC	TCC	TGC	TCA	TCT	GCT	TTG	GCC	TCG	AAG	CCC	AGC	CCA	1248
Ser	Glu	Ala	Ser	Ser	Cys	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Pro	Ser	Pro	
			405					410						415		
GAG	GGA	GCC	TCT	GCT	GCC	AGC	TTT	GAG	TAC	ACT	ATC	CTG	GAC	CCC	AGC	1296
Glu	Gly	Ala	Ser	Ala	Ala	Ser	Phe	Glu	Tyr	Thr	Ile	Leu	Asp	Pro	Ser	
			420					425					430			
TCC	CAG	CTC	TTG	CGT	CCA	TGG	ACA	CTG	TGC	CCT	GAG	CTG	CCC	CCT	ACC	1344
Ser	Gln	Leu	Leu	Arg	Pro	Trp	Thr	Leu	Cys	Pro	Glu	Leu	Pro	Pro	Thr	
		435				440						445				
CCA	CCC	CAC	CTA	AAG	TAC	CTG	TAC	CTT	GTG	GTA	TCT	GAC	TCT	GGC	ATC	1392
Pro	Pro	His	Leu	Lys	Tyr	Leu	Tyr	Leu	Val	Val	Ser	Asp	Ser	Gly	Ile	
	450					455					460					
TCA	ACT	GAC	TAC	AGC	TCA	GGG	GAC	TCC	CAG	GGA	GCC	CAA	GGG	GGC	TTA	1440
Ser	Thr	Asp	Tyr	Ser	Ser	Gly	Asp	Ser	Gln	Gly	Ala	Gln	Gly	Gly	Leu	
	465				470				475						480	
TCC	GAT	GGG	CCC	TAC	TCC	AAC	CCT	TAT	GAG	AAC	AGC	CTT	ATC	CCA	GCC	1488
Ser	Asp	Gly	Pro	Tyr	Ser	Asn	Pro	Tyr	Glu	Asn	Ser	Leu	Ile	Pro	Ala	
				485				490						495		
GCT	GAG	CCT	CTG	CCC	CCC	AGC	TAT	GTG	GCT	TGC	TCT	TAG				1527
Ala	Glu	Pro	Leu	Pro	Pro	Ser	Tyr	Val	Ala	Cys	Ser					
			500					505								

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asp	His	Leu	Gly	Ala	Ser	Leu	Trp	Pro	Gln	Val	Gly	Ser	Leu	Cys	
1				5				10						15		
Leu	Leu	Leu	Ala	Gly	Ala	Ala	Trp	Ala	Pro	Pro	Pro	Asn	Leu	Pro	Asp	
			20				25						30			
Pro	Lys	Phe	Glu	Ser	Lys	Ala	Ala	Leu	Leu	Ala	Ala	Arg	Gly	Pro	Glu	
	35					40					45					

Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
 50 55 60
 Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
 65 70 75 80
 Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
 85 90 95
 Pro Thr Ala Arg Gly Arg Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
 100 105 110
 Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser
 115 120 125
 Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu
 130 135 140
 Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly
 145 150 155 160
 His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser
 165 170 175
 His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Arg Pro Gly Ser
 180 185 190
 Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser
 195 200 205
 Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Arg Ala Arg Met
 210 215 220
 Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val
 225 230 235 240
 Ser Leu Leu Glu Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser
 245 250 255
 Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu
 260 265 270
 Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser
 275 280 285
 Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe
 290 295 300
 Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys
 305 310 315 320
 Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu
 325 330 335
 Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu
 340 345 350
 Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr
 355 360 365
 Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp
 370 375 380

Leu Pro Gly Pro Gly Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly
 385 390 395 400
 Ser Glu Ala Ser Ser Cys Ser Ser Ala Leu Ala Ser Lys Pro Ser Pro
 405 410 415
 Glu Gly Ala Ser Ala Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser
 420 425 430
 Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr
 435 440 445
 Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile
 450 455 460
 Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu
 465 470 475 480
 Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala
 485 490 495
 Ala Glu Pro Leu Pro Pro Ser Tyr Val Ala Cys Ser
 500 505